

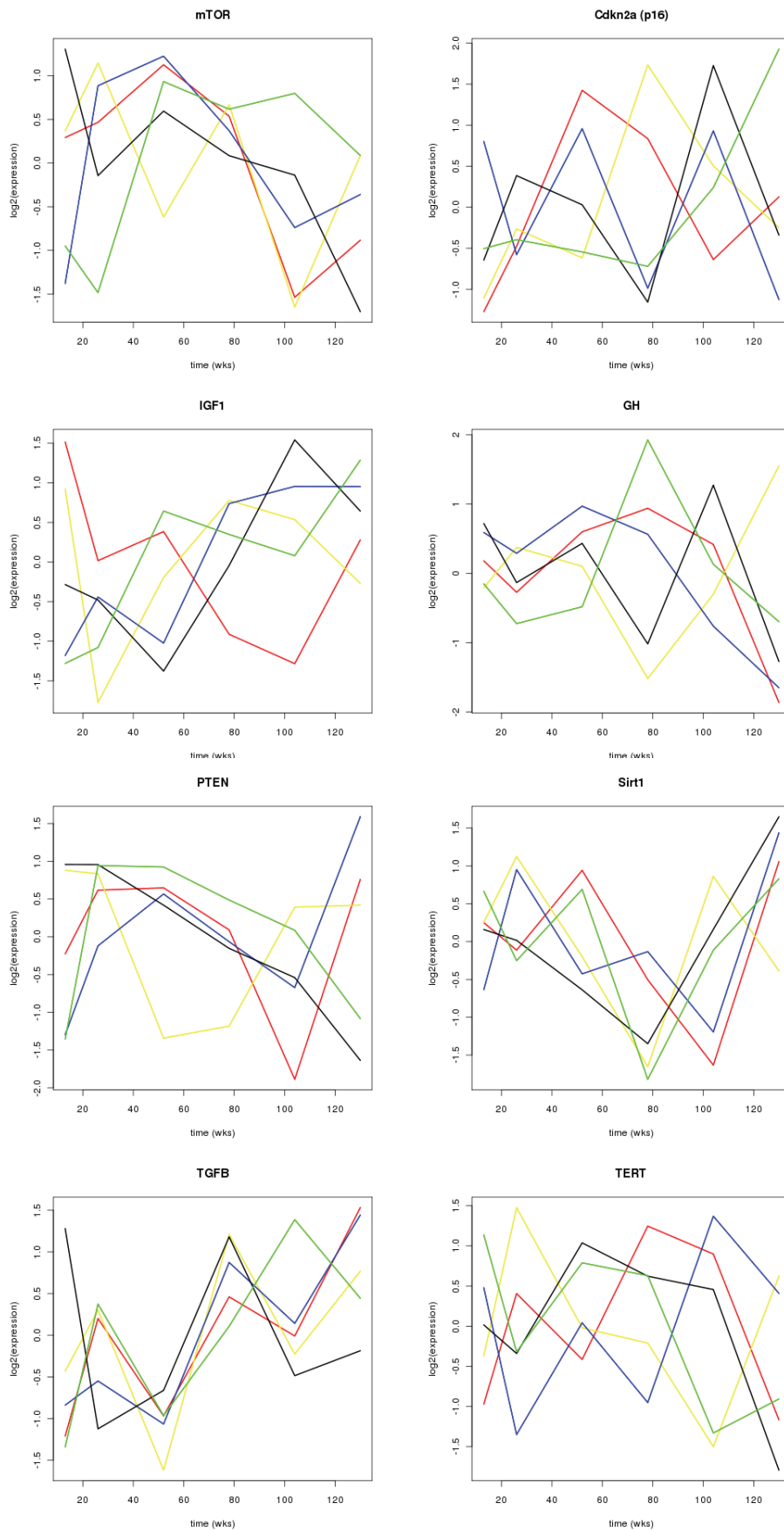
Supplemental information 03.

Scatter plot depicting the samples plotted against the first two principal components calculated from the intensities of the perfect match probes. The colors indicate liver (yellow), kidney (blue), spleen (green), lung (grey), brain (red). The numbers indicate the age of each sample (in weeks.)

Supplemental Information 04. List of genes that were differentially expressed (FDR corrected p-values and q-values (FDR adjusted p-values) are listed, indicating the degree of significance. A: DEGs are ordered based on q-value, and q-values < 0.050 are marked green. The visible overlap is shown in green. B: Expression profiles during aging in all organs of the only gene that is significantly differentially expressed.

l value ≤ 0.05) in any of the organs
nce of differential expression of all DEGs during aging.
nmarized in SI06.
ssed in all five organs examined: Lilrb4 (Affymetrix probe-set identifier 1420394_s_at)

Supplemental information 05. Dynamics of several literature based age-related genes during murine lifespan. Liver (red), kidney (blue), spleen (black), lung (yellow) and brain (green).



Supplemental Information 06. The organ intersections in differentially expressed genes (DEGs) (SI04) and functionally related altered gene sets (AGSs) (SI07).

	Organ	DEGs	AGSs
	liver	6,973	122
	kidney	2,325	203
	spleen	925	307
	lung	1,025	59
	brain	15	82
Overlap	Organ combinations	DEGs	AGSs
Specific	liver	5,886	63
	kidney	1,533	118
	spleen	588	164
	lung	679	16
	brain	5	20
	<i>subtotal</i>	<i>8,691</i>	<i>381</i>
Two	liver; kidney	594	8
	liver; spleen	219	14
	liver; lung	177	5
	liver; brain	3	0
	kidney; spleen	40	10
	kidney; lung	76	3
	kidney; brain	0	8
	spleen; lung	25	3
	spleen; brain	0	11
lung; brain	0	13	
	<i>subtotal</i>	<i>1,134</i>	<i>75</i>
Three	liver; kidney; spleen	24	1
	liver; kidney; lung	41	0
	liver; kidney; brain	3	0
	liver; spleen; lung	12	1
	liver; spleen; brain	2	0
	liver; lung; brain	0	0
	kidney; spleen; lung	3	5
	kidney; spleen; brain	0	10
	kidney; lung; brain	0	3
	spleen; lung; brain	0	0
	<i>subtotal</i>	<i>85</i>	<i>20</i>
Four	liver; kidney; spleen; lung	10	0
	liver; kidney; spleen; brain	0	0
	liver; spleen; lung; brain	1	0
	liver; kidney; lung; brain	0	2
	kidney; spleen; lung; brain	0	4
	<i>subtotal</i>	<i>11</i>	<i>6</i>
Generic	liver; kidney; spleen; lung; brain	1	0
	<i>subtotal</i>	<i>1</i>	<i>0</i>
	<i>total</i>	<i>9,922</i>	<i>482</i>

Supplemental Information 07. Lists of altered gene sets (AGSs) that were found to be involved

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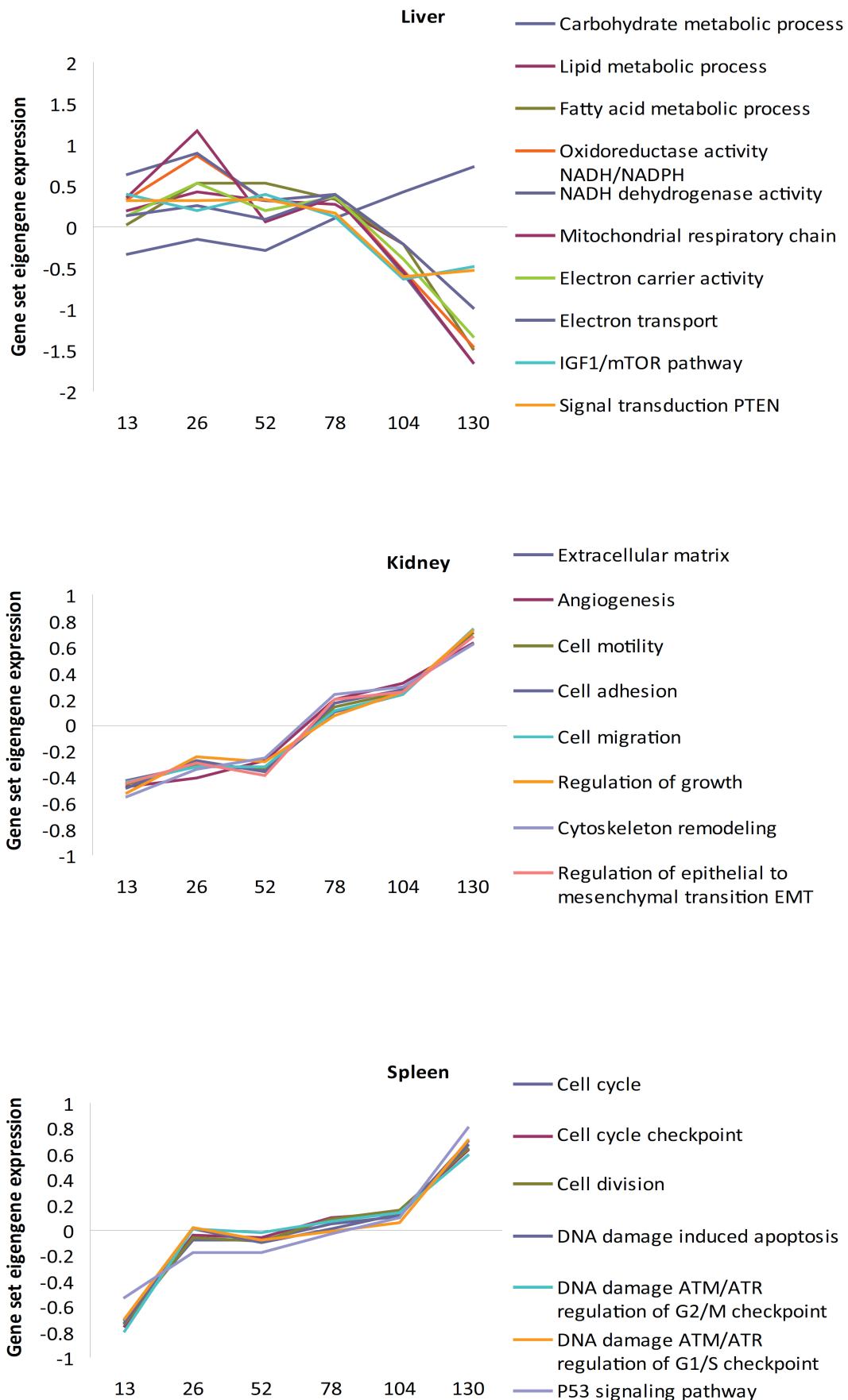
in aging in the different organs after gene set analysis (GSA) overrepresentation analysis (ORA)

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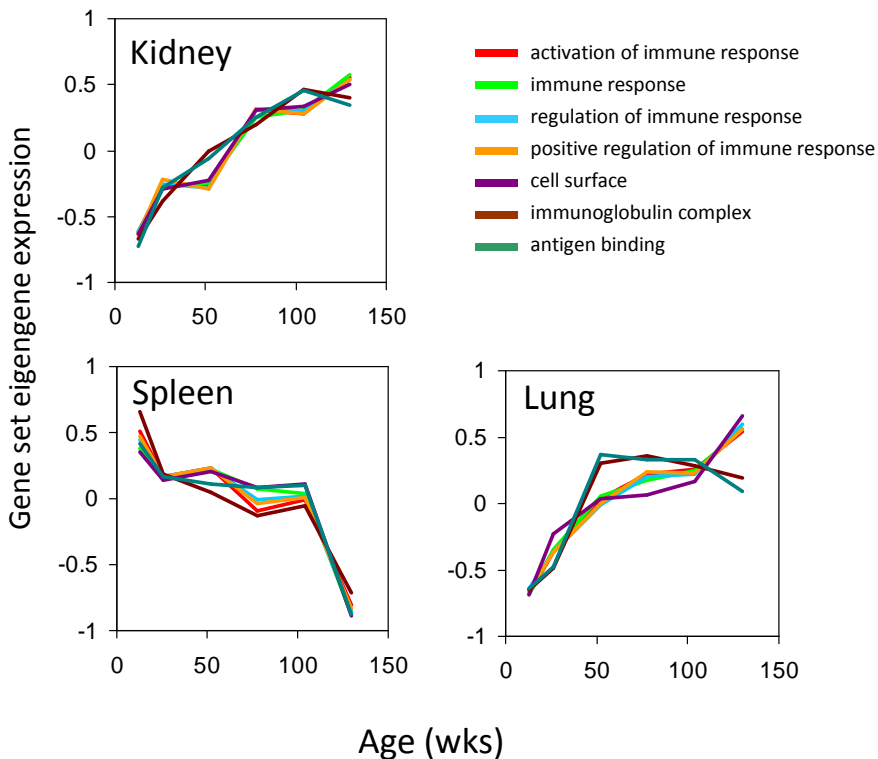
and Metacore overrepresentation analysis (M-ORA).

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Supplemental information 08. Dynamics of average, age-related gene expression changes of selected organ-specific, overrepresented gene sets.



Supplemental information 09. Organ-specific gene expression dynamics of common immune related gene sets in kidney, spleen, and lung.



Supplemental Information 10. List of genes that showed significant correlation (p-value ≤ 0.001) with
The p-values of the correlation (cor) and partial correlation, which includes a correction for chronology
The union of the correlated and partial correlated genes per pathological parameter are presented in Table 1

th any pathological parameter in any of the organs.
ical age, (pcor) are shown.

Supplemental Information 11. Lists of altered gene sets (AGSs) correlated to the pathological
1= Found as an AGS (green). Grey cells indicate processes also present as an AGS in chronolog

parameters in five organs after gene set analysis (GSA), overrepresentation analysis (ORA) and
gical ginga

l Metacore overrepresentation analysis (M-ORA). If present, overlap with chronologi

Supplemental information 12. Predefined list of aging related gene-sets based on literature.

Source	Gene set	# genes
Gene Ontology	aging_GO:0007568	24
Gene Ontology	cell aging_GO:0007569	10
Gene Ontology	multicellular organismal aging_GO:0010259	7
Gene Ontology	response to reactive oxygen species_GO:0000302	16
Gene Ontology	response to hydrogen peroxide_GO:0042542	10
Gene Ontology	response to oxygen radical_GO:0000305	5
Gene Ontology	DNA repair_GO:0006281	177
Gene Ontology	base-excision repair_GO:0006284	16
Gene Ontology	double-strand break repair_GO:0006302	18
Gene Ontology	mismatch repair_GO:0006298	9
Gene Ontology	non-recombinational repair_GO:0000726	6
Gene Ontology	nucleotide-excision repair_GO:0006289	22
Gene Ontology	recombinational repair_GO:0000725	6
Gene Ontology	telomere maintenance_GO:0000723	17
Gene Ontology	response to oxidative stress_GO:0006979	45
Joost	Energy_restriction_and_the_GH.IGF.1_axis	13
Joost	DNA_metabolism	30
Joost	Oxidant_levels_and_redox_potential	18
Joost	Stress_response	5
BIOCARTA	ARENRF2_PATHWAY	14
BIOCARTA	INFLAM_PATHWAY	26
BIOCARTA	DEATH_PATHWAY	30
BIOCARTA	LONGEVITY_PATHWAY	15
BIOCARTA	STRESS_PATHWAY	25
BIOCARTA	WNT_PATHWAY	25
BIOCARTA	P53_PATHWAY	16
BIOCARTA	NFKB_PATHWAY	22
BIOCARTA	IGF1MTOR_PATHWAY	19
BIOCARTA	IGF1_PATHWAY	22
BIOCARTA	MTOR_PATHWAY	23
KEGG	OXIDATIVE_PHOSPHORYLATION	110
KEGG	MTOR_SIGNALING_PATHWAY	52
KEGG	BASE_EXCISION_REPAIR	30
KEGG	NUCLEOTIDE_EXCISION_REPAIR	43
KEGG	MISMATCH_REPAIR	22
KEGG	WNT_SIGNALING_PATHWAY	148
REACTOME	BASE_EXCISION_REPAIR	16
REACTOME	CELL_DEATH_SIGNALLING_VIA_NRAGE_NRIF_AND_NADE	54
REACTOME	DEATH_RECEPTOR_SIGNALLING	11
REACTOME	DNA_REPAIR	82
REACTOME	DOUBLE_STRAND_BREAK_REPAIR	19
REACTOME	EXTENSION_OF_TELOMERES	23
REACTOME	SIGNALING_BY_WNT	16
REACTOME	SYNTHESIS_OF_DNA	46
REACTOME	TELOMERE_MAINTENANCE_hs	37
REACTOME	APOPTOSIS	82
REACTOME	ENERGY_DEPENDENT_REGULATION_OF_MTOR_BY_LKB1_AMPK	12
REACTOME	MTOR_SIGNALLING	22
REACTOME	MTORC1_MEDIATED_SIGNALLING	10